



114: Assessing a polygenic risk score for Parkinson's disease in 22q11.2 deletion syndrome

Nikolai Gil D. Reyes^{1,2,3,4}, Shengjie Ying^{2,3}, Adrian I. Espiritu⁵, Tracy Heung^{2,3}, Yue Yin⁶, Erik Boot^{7,8}, Anthony E. Lang^{4,9}, Connie Marras⁴, Ryan K.C. Yuen^{6,10}, Anne S. Bassett^{1,2,3,11}

¹*Institute of Medical Science, Temerty Faculty of Medicine, University of Toronto, Toronto, ON, Canada;* ²*Dalglish Family 22q Clinic, Toronto General Hospital, Toronto, ON, Canada;* ³*Clinical Genetics Research Program, Centre for Addiction & Mental Health, Toronto, ON, Canada;* ⁴*Edmond J. Safra Program in Parkinson's Disease, the Rossy Progressive Supranuclear Palsy Centre, and the Morton and Gloria Shulman Movement Disorders Clinic, Toronto Western Hospital, Toronto, ON, Canada;* ⁵*Department of Neurosciences, University of the Philippines-Philippine General Hospital, Manila, Philippines;* ⁶*Genetics and Genome Biology, The Hospital for Sick Children; Toronto, ON, Canada;* ⁷*Advism, 's Heeren Loo Zorggroep, Amersfoort, The Netherlands;* ⁸*Department of Psychiatry and Neuropsychology, Mental Health and Neuroscience Institute (MHeN)s, Maastricht University, Maastricht, The Netherlands;* ⁹*Krembil Research Institute, Toronto Western Hospital, Toronto, ON, Canada;* ¹⁰*Department of Molecular Genetics, University of Toronto; Toronto, ON, Canada;* ¹¹*Department of Psychiatry, University of Toronto, Toronto General Hospital Research Institute, and Campbell Family Mental Health Research Institute, Toronto, ON, Canada.*

Background: The 22q11.2 microdeletion confers an elevated risk of parkinsonism, particularly early-onset Parkinson's disease (PD). The extent to which common genetic variation associated with idiopathic PD modifies parkinsonism risk in 22q11.2 deletion syndrome (22q11.2DS) remains unclear. **Methods:** We performed an out-of-sample PD polygenic risk score (PD-PRS) analysis in 205 unrelated adults with a typical 22q11.2 microdeletion (31 parkinsonism-cases, 174 controls) with available genome sequencing and movement disorder phenotype data. Allele-weighted risk scores were calculated in PLINK using a previously validated PD-PRS (PGS000903) comprising 1,392 single nucleotide polymorphisms (SNPs). Between-group comparisons were conducted in the full sample and in an age-adjusted subsample (controls ≥ 30 years). Association between PD-PRS and parkinsonism status was evaluated using logistic regression models adjusting for age, ancestry, and psychotic illness. Sensitivity analyses were performed using a genome-wide significant 90-variant PD-PRS (PGS000902; 37 overlapping SNPs). **Results:** Standardized PD-PRS did not differ significantly between individuals with and without parkinsonism in the full sample ($p = 0.85$) or age-adjusted sample ($p = 0.96$). Logistic regression revealed no significant association between PD-PRS and parkinsonism (unadjusted OR 0.96, 95% CI 0.66–1.41; adjusted OR 0.90, 95% CI 0.53–1.53; p for both models >0.5). Inclusion of PD-PRS in the full model increased explained variance by $<2\%$ ($\Delta\text{Nagelkerke } R^2 \leq 0.002$). Findings were consistent using the 90-variant PD-PRS. **Conclusions:** Interim analyses suggest the possibility that PD-PRS derived from a large population-based GWAS does not significantly modify parkinsonism risk in adults with a typical 22q11.2 microdeletion. These preliminary findings may indicate that PD-associated common genetic variation contribute minimally to motor expression in the presence of a high-impact variant such as 22q11.2 microdeletion. The genetic architecture of 22q11.2DS-associated (early-onset) parkinsonism may differ from that of idiopathic (late-onset) PD. Our findings support investigation of alternative genetic risk modifiers, including additional rare variants.